

EXHIBIT B

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	10	20	30	40	50	60
SEQID14	-----					
SEQID15	-----					
SEQID13	MAADGYLPDWLEDYLSEGIRQWWKLKPGPPPKPAERHKDDSRGLVLPGYKYLGPFGNLD					
Prim. cons.	MAADGYLPDWLEDYLSEGIRQWWKLKPGPPPKPAERHKDDSRGLVLPGYKYLGPFGNLD					
	70	80	90	100	110	120
SEQID14	-----					
SEQID15	-----					
SEQID13	KGSPVNEADAALEHDKAYDRQLSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ					
Prim. cons.	KGEPVNEADAALEHDKAYDRQLSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ					
	130	140	150	160	170	180
SEQID14	-----MAPGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
SEQID15	-----					
SEQID13	AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
Prim. cons.	AKKRVLEPLGLVEEPVK2APGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
	190	200	210	220	230	240
SEQID14	SVPDPQPLGQPPAAPSGLGTNTMATGSGAPMADNNNEGADGVGNSSGNWHCDSTWMGDRV					
SEQID15	-----MATGSGAPMADNNNEGADGVGNSSGNWHCDSTWMGDRV					
SEQID13	SVPDPQPLGQPPAAPSGLGTNTMATGSGAPMADNNNEGADGVGNSSGNWHCDSTWMGDRV *****					
Prim. cons.	SVPDPQPLGQPPAAPSGLGTNTMATGSGAPMADNNNEGADGVGNSSGNWHCDSTWMGDRV					
	250	260	270	280	290	300
SEQID14	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPwgYFDFNRFHCHFSPRDWQRLI					
SEQID15	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPwgYFDFNRFHCHFSPRDWQRLI					
SEQID13	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPwgYFDFNRFHCHFSPRDWQRLI *****					
Prim. cons.	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPwgYFDFNRFHCHFSPRDWQRLI					
	310	320	330	340	350	360
SEQID14	NNNWGFRPKRLNPKLFNIQVKEVTONDGTITIANNLTSTVQVFTDSEYQLPYVLGSAHQG					
SEQID15	NNNWGFRPKRLNPKLFNIQVKEVTONDGTITIANNLTSTVQVFTDSEYQLPYVLGSAHQG					
SEQID13	NNNWGFRPKRLNPKLFNIQVKEVTONDGTITIANNLTSTVQVFTDSEYQLPYVLGSAHQG *****					
Prim. cons.	NNNWGFRPKRLNPKLFNIQVKEVTONDGTITIANNLTSTVQVFTDSEYQLPYVLGSAHQG					
	370	380	390	400	410	420
SEQID14	CLPPPFPADVFMPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNPTFSYTFEDVPF					
SEQID15	CLPPPFPADVFMPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNPTFSYTFEDVPF					
SEQID13	CLPPPFPADVFMPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNPTFSYTFEDVPF *****					
Prim. cons.	CLPPPFPADVFMPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNPTFSYTFEDVPF					

	430	440	450	460	470	480
SEQID14	HSSYAHQSLSLRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPG					
SEQID15	HSSYAHQSLSLRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPG					
SEQID13	HSSYAHQSLSLRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPG					
Prim. cons.	HSSYAHQSLSLRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPG					
	490	500	510	520	530	540
SEQID14	PCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSLVPGPAMASHKDDDEKKFFPQSGVL					
SEQID15	PCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSLVPGPAMASHKDDDEKKFFPQSGVL					
SEQID13	PCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSLVPGPAMASHKDDDEKKFFPQSGVL					
Prim. cons.	PCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSLVPGPAMASHKDDDEKKFFPQSGVL					
	550	560	570	580	590	600
SEQID14	IFGKQGSEKTNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGV					
SEQID15	IFGKQGSEKTNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGV					
SEQID13	IFGKQGSEKTNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGV					
Prim. cons.	IFGKQGSEKTNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGV					
	610	620	630	640	650	660
SEQID14	LPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPPLMGGFGLKHPPPQILIKNTPV PANPSTT					
SEQID15	LPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPPLMGGFGLKHPPPQILIKNTPV PANPSTT					
SEQID13	LPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPPLMGGFGLKHPPPQILIKNTPV PANPSTT					
Prim. cons.	LPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPPLMGGFGLKHPPPQILIKNTPV PANPSTT					
	670	680	690	700	710	720
SEQID14	FSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQTSNYNKSVNVDFTVDTNGVY					
SEQID15	FSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQTSNYNKSVNVDFTVDTNGVY					
SEQID13	FSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQTSNYNKSVNVDFTVDTNGVY					
Prim. cons.	FSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQTSNYNKSVNVDFTVDTNGVY					
	730					
SEQID14	SEPRPIGTRYLTRNL					
SEQID15	SEPRPIGTRYLTRNL					
SEQID13	SEPRPIGTRYLTRNL					
Prim. cons.	SEPRPIGTRYLTRNL					

Alignment data :

Alignment length : 735

Identity (*) : 533 is 72.52 %

Strongly similar (:) : 0 is 0.00 %

Weakly similar (.) : 0 is 0.00 %

Different : 202 is 27.48 %

Sequence 0001 : SEQID14 (598 residues). VP2

Sequence 0002 : SEQID15 (533 residues). VP3

Sequence 0003 : SEQID13 (735 residues). VP1

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